

1001 GTCAACACTA CTGTTGCCCTT AAGCTGCACC TGCCGAGGCA GCGGCAACCT ACAGGACGAG TGTGAACAGC TGGAAAAGGTC CTTCTCCCAG AACCCCTGCC
CAGTTGTGAT GACAAACGGAA TTCGACGFGG ACGGCTCCGT CGCGTTTGA TGCTGCTC ACCTTTCCAG GAAGAGGTC TTGGGGACGG
305 ValAsnThrT hrValAlaLe userCysThr CysArgGlys erGlyAsnLe uGlnAspGlu CysGluGlnL euGluArgSe rPheSerGln AsnProCysLeu
1101 TCGTGGAGGC CATTGCAGCT AAGATGCGTT TCCACAGACA GCTCTTCTCC CAGGACTGGG CAGACTCTAC TTTTTCAGTG GTGCAGCAGC AGAACAGCAA
AGCACCTCCG GTAACGTCGA TTCTACGCAA AGGTGCTGTG CGAGAAGAGG GTCCTGACCC GTCTGAGATG AAAAAGTCAC CACGTCGTCG TCTTGTCTGT
339 ValGluAl aileAlaAla LysMetArgP heHisArgG1 nLeuPheSer GlnAspTrpA laAspSerVal ValGlnGlnG InAsnSerAsn
1201 CCCTGCTCTG AGACTGCAGC CCAGGCTACC CATTCTTTCT TTCTCCATCC TTCCCTTGAT TCTGCTGCAG ACCCTCTGGT AGCTGGGCTT CCTCAGGGTC
GGGACGAGAC TCTGACGTCG GGTCCGATGG GTAAGAAAGA AAGAGGTAGG AAGGGAATA AGACGACGTC TGGGAGACCA TCGACCCGAA GGAGTCCCAG
372 ProAlaLeu ArgLeuGlnP roArgLeuPr oileLeuSer PheSerIleL euProLeuI eLeuLeuGln ThrLeuTrp
1301 CTTTGTCTC TCCACCACAC CCAGACTGAT TTGCAGCCTG TGGTGGGAGA GAACTCGCCA GCCTGTGGAA GAAGACGCAG CGTGCTACAC AGCAACCCCG
GAAACAGGAG AGGTGGTGTG GGTCTGACTA AACGTCGGAC ACCACCTCT CTTGAGCGGT CGGACACCTT CTTCGCGTC GCACGATGTG TCGTTGGGCC
1401 AACCAACCAG GCATTCCGCA GCACATCCCG TCTGCTCCAG AAGAGTCTT AGAAGTGAGG GCTGTGACCC TTCCGATCCT GAGCGGCTAG TTTTCAAACC
TTGGTTGCTC CGTAAGCGT CGTGTAGGC AGACGAGGTC TTCTCCAGAA TCCTCACTCC CGACACTGGG AAGGCTAGGA CTCGCCGATC AAAAGTTTGG
1501 TCCCTTGCCC CTGCTTCTCT CTGGCTCAGG CTGCTCCTCC TTAGGACTTT GTGGGTCCAG TTTTGCCTTC TGTTCGTGATG GTGATTAGCG GCTCACCTCC
AGGGAACGGG GACGAAGGAA GACCGAGTCC GACGAGGAGG AATCCTGAAA CACCCAGGTC AAAACGGAG ACAAGACTAC CACTAATCGC CGAGTGGAGG
1601 AGCGCTTCTT CCTGTTTCCC AGGACCACCC AGAGGCTAAG GAATCAGTCA TTCCCTCTTG CTTCTCTCCAG GAAGGCAGGC TAAGGGTTCT GAGGTGACTG
TCGCGAAGAA GGACAAAGG TCCTGGTGGG TCTCCGATT CTTAGTCAGT AAGGGACAAC GGAAGAGGTC CTTCCGTCCG ATTCCCAGA CTCCACTGAC
1701 AGAAAAATGT TTCCTTTGTG TGAAGGCTG GTGCTCCAGC CTCACGTCCT CTCTGAATGG AAGATAAAA CCTGCTGGTG TCTTGACTGC TCTGCCAGGC
TCTTTTTCACA AAGGAAACAC ACCTTCCGAC CACGAGGTG CACGAGGTG GAGGTGACG GAGACTTACC TTCTATTTTT GGACGACCAC AGAAGTACG AGACGGTCCG
1801 AATCCTGAAC ATTTGGGCAT GAAGAGCTAA AGTCTTTGGG TCTTGTTTAA CTCCTATTAC CTCCTCCCAA TTCCCTTAGT CCCTTGGGTC ATGATTAAAC
TTAGGACTTG TAAACCCGTA CTTCTCGATT TCAGAAACCC AGAACAAATT GAGGATAATG ACAGGGTTT AAGGGGATCA GGAACCCAG TACTAATTG
1901 ATTTTGACTT AAAAAAAA AAAAAAAA AAAAAA
TAAACTGAA TTTTTTTTTT TTTTTTTTTT TTTTT

FIG. 1B

FIG. 2

hGFra3	1	M	V	R	P	L	N	P	R	P	L	P	P	V	V	L	M	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L	L
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FIG. 3

48613 1 MVRPLNPRPLPPVVLMLLLPPSPPLPLAAGDPLPTESRLMNSCLQARRK
48614 1 MVRPLNPRPLPPVVLMLLLPPSPPLPLAAGDPLPTESRLMNSCLQARRK

48613 51 QADPTCSAAYHHLDSTSSISTPLPSEEPSVPADCLEAAQQLRNSSLIG
48614 51 QADPTCSAAYHHLDSTSSISTPLPSEEPSVPADCLEAAQQLRNSSLIG

48613 101 CMCHRRMKNQVACLDIYWTVHRARSLGNYELDVSPYEDT VTSKPWKMNLS
48614 101 CMCHRRMKNQVACLDIYWTVHRARSL

48613 151 KLNMLKPPDSDLCLKFAMLCTLNDKCDRLRKAYGEACSGPHCQRHVCLRQL
48614 127 DSDLCLKFAMLCTLNDKCDRLRKAYGEACSGPHCQRHVCLRQL

48613 201 LTFEKEAAEPHAQGLLLCPCAPNDRGCGERRRNTIAPNCALPPVAPNCLE
48614 170 LTFEKEAAEPHAQGLLLCPCAPNDRGCGERRRNTIAPNCALPPVAPNCLE

48613 251 LRRLCFSDPLCRSRLVDFQTHCHPMDILGTCATEQSRCLRAYLGLIGTAM
48614 220 LRRLCFSDPLCRSRLVDFQTHCHPMDILGTCATEQSRCLRAYLGLIGTAM

48613 301 TPNFVSNVNTSVALSCTCRGSGNLQEECEMLEGFFSHNPCLTEAIAAKMR
48614 270 TPNFVSNVNTSVALSCTCRGSGNLQEECEMLEGFFSHNPCLTEAIAAKMR

48613 351 FHSQLFSQDWPHPPTFAVMAHQENPAVRQPWPVPSLFSC TLP L I L L S L W
48614 320 FHSQLFSQDWPHPPTFAVMAHQENPAVRQPWPVPSLFSC TLP L I L L S L W

FIG. 4

DNA48613.orf 1 A T G G T G C G C C C C C T G A A C C G C G A C C G C T G C C G C C C G T A G T C T G A T G T T
GENFRa1.orf 1 A T G A T C T T G G C A A A C G T C T T C T G C T C T T C T T C T T C T T
GENFRa2.orf 1 A T G A T C T T G G C A A A C G T C T T C T G C T C T T C T T C T T C T T

DNA48613.orf 51 G C T G C T G C T G C T G C C G C T G C C T C T C G C A G C C G A G A C C C C C
GENFRa1.orf 6 C C T G G C G A C C C T G T A C T T C G C G C T G C C G C T C T T G G A C T T G C T C C T G T C G G
GENFRa2.orf 39 A G A C G A G A C C C T C G C T C T T T G G C C A G C C C T T C C T C C T G C A G G C C C G

DNA48613.orf 101 T T C C A C A G A A G C C G A C T C A T G A A C A G C T G T C T C C A G G C C A G G A G A G
GENFRa1.orf 56 C C G A A G T G A G C G G G A G A C C G C C T G G A T T G C G T G A A G C C A G T G A T C A G
GENFRa2.orf 89 A G C T C A C G G C T G G C G C C C C A G T G G A C T G T C C G G G C C A A T G A G C T G

DNA48613.orf 151 T G C C A G G C T G A T C C C A C C T G C A G T G C T A C C A C C A C C T G G A T T C C T G
GENFRa1.orf 106 T G C C T G A A G G A G C A G A G C T G C A G C A C A A G T A C C G C A C G C T A A G G C A G T G
GENFRa2.orf 139 T G T G C C G C C G A T C C A A C T G C A G C T C T C G C T A C C G C A C T C T G C G C A G T G

DNA48613.orf 201 C A C C T C T A G C A T A A G C A C C C C A C T G C C C T . . . C A G A G A G C C T T C G G T C C
GENFRa1.orf 156 C G T G C C G G C A A G G A G A C C A A C T T C A G C C T G G C A T C C G G C C T G G A G G C C A
GENFRa2.orf 189 C C T G G C A G G C C G C G A C C G C A C A C C A T G C T G G C C A

DNA48613.orf 248 C T G C T G A C T G C C T G G A G G C A G C A G C A C T C A G G A C A G C T C T G A T A
GENFRa1.orf 206 A G A T G A G T G C C G C A G C G C C A T G G A G G C C C T G A A G C A G A A G T C G C T C T A C
GENFRa2.orf 224 A C A G G A G T G C C A G G C G C C T T G G A G G T C T T G C A G G A G A G C C C G C T G T A C

DNA48613.orf 298 G G C T G C A T G T G C C A C C G G C G C A T G A A G A A C C A G G T T G C T G C T T G G A C A T
GENFRa1.orf 256 A C T G C C G C T G C A A G C G G G T A T G A A G A A G G A A A G A A C T G C C T G C G C A T
GENFRa2.orf 274 G A C T G C C G C T G C A A G C G G G G C A T G A A G A A G G A G C T G C A G T G T C T G C A G A T

DNA48613.orf 348 C T A T T G G A C C G T T C A C C G T G C C G C A G C C T T G G T A A C T A T G A G C T G G A T G
GENFRa1.orf 306 T T A C T G G A G C A T G T A C C A G A C C T G C A G G G A A A T G A T C T G T G G A G G A T T
GENFRa2.orf 324 C T A C T G G A G C A T C A C C T G G G C T G A C C G A G G T G A G G A G T T C T A C G A G

FIG. 5A

DNA48613.orf 398 TCTCCCCCTATGAAG.....ACACAGTGAACAGC
 GDNFRa1.orf 356 CC[C]ATATGAACCAAGTTA.....ACAGCAGGATTGTCA
 GDNFRa2.orf 374 CCTCCCCCTATGAGCCGGTGACCTCCCGCCTCTCGGACATCTTCAAGCTT

DNA48613.orf 427 AAAC[CT]GGAAATGAATCTCAGCAAACTGAACAATGCTCAAAACAGACTC
 GDNFRa1.orf 388 GATATATTCCGGGTGGTCCCAATTCATATCAGTGGAGCAATTCCCAAAGG
 GDNFRa2.orf 424 GC[T]CAATCTTCTCAGGGACAAGGGCAAGACCCGGTGGTCAAGCGCCAAAGAG

DNA48613.orf 477 AGACCTCTGCCTCAAGTTTGGCAATGCTGTGT[ACT]CTCAATGACAAAGTGTG
 GDNFRa1.orf 438 GAAACAACCTGCCTGGATGCAAGCGAAGGCCCTGCAACCTC[GA]CGACATTTGCA
 GDNFRa2.orf 474 CAACCATTGCCTGGATGCTGCCAAGGCCCTGCAACCTTGAATGACAACTGCA

DNA48613.orf 527 ACCGGCTGCGCAAGGCCCTACGGGGAGGCGGTGCTCCGGGCCCACTG...C
 GDNFRa1.orf 488 AGAAGTACAAGTCCGGCGTACATCAACCGTGCACCAACAGCGTGTCT...C
 GDNFRa2.orf 524 AGAAGCTGCGCTCTCTACATCTCCATCTGCAACCGCGAGATCTCGCCC

DNA48613.orf 574 CAGGCGCA[CGTCT]GCTCAAGCAAGCTGCTCACTTTCTTCGAGAAGGCCGCGC
 GDNFRa1.orf 535 AATGATGTCTGCAACCGCCGCAAGTGCCACAAGGCCCTCCGGCAGTTCTT
 GDNFRa2.orf 574 ACCGAAGCGCTGCAACCGCCGCAAGTGCCACAAGGCCCTGCGCAGTTCTT

DNA48613.orf 624 C G A G C C C C A C G C G C A G G C C T G C T A C T G T G C C A T G T G C C C C A
 GDNFRa1.orf 585 T G A C A A G G T C C G G C C A G C A C A G C T A C G G A A T G C T C T T C T G C T C C T G C C
 GDNFRa2.orf 624 C G A C C G G T G C C C A G C G A G T A C A C T A C C G C A T G C T C T T C T G C T C C T G C C

DNA48613.orf 688 A C G A C C G G G C T G C G G G A G G C C C G G C A C A C C A T C G C C C A A C T G C
 GDNFRa1.orf 635 G G G A C A T C G C C T G C A C A G A G C G A G C C A T C G T G C C T G T G C
 GDNFRa2.orf 674 A A G A C C A G G C G T G C G C T G A G C G C C G C C G G C A A C C A T C C T G C C C A G C T G C

FIG. 5B

DNA48613.orf 718 G C G C T G C C . . . G C C T G T G G C C C C C A A C T G C C T G G A G C T G C G G G C G C T C T G
GENFRa1.orf 585 T C C T A T G A A G A G A G G A G A G C C C A A C T G T T G A A T T T G C A G G A C T C C T G
GENFRa2.orf 724 T C C T A T G A G G A C A A G G A A G C C C A A C T G C C T G G A C T G C G T G G C G T G T G

DNA48613.orf 765 C T T C T C G A C C C G C T T T G C A G A T C A C G C C T G G T G G A T T T C C A G A C C C A C T
GENFRa1.orf 735 C A G A C G A A T T A C A T C T G C A G A T C T C G C C T T G C G G A T T T T T A C C A A C T
GENFRa2.orf 774 C C G G A C T G A C C A C C T G T G T C G G T C C G G C T G G C C G A C T T C C A T G C C A A T T

DNA48613.orf 815 G C C A T C C C A T G G A C A T C C T A G G A A C T T G T G C A A C A G A G C A G T C C A G A . . .
GENFRa1.orf 785 G C C A G C C A G A T C A A G T C T G T C A G C A G C T G T C T A A A G G A A A C T A C G C T
GENFRa2.orf 824 G T C G A G C C T C C T A C C A G A C G G T C A C C A G C T G C C C T G C G G A C A A T T A C C A G

DNA48613.orf 862 . . . T G T C T A C G A G C A T A C C T G G G G C T G A T T G G G A C T G C C A T G A C C C C C A A
GENFRa1.orf 835 G A C T G C C T C C T C G C C T A C T C G G G G C T T A T T G G C A C A G T C A T G A C C C C C A A
GENFRa2.orf 874 G C G T G T C T G G C T C T A T G C T G G C A T G A T T G G G T T G A C A T G A C A C C T A A

DNA48613.orf 909 C T T T G T C A G C A A T G T C A A C A C C A G T G T T G C C T T A A G C T G C A C C T
GENFRa1.orf 885 C T A C A T A G A C T C C A G T A G C C T C A G T G T G G C C C C A T G G T G T G A C T
GENFRa2.orf 924 C T A T G T G G A C T C C A G C C C A C T G G C A T C G T G T G T C C C C C T G G T G C A G C T

DNA48613.orf 953 G C C G A G G C A G T G G C A A C C T G C A G G A G G A G T G T G A A A T G C T G G A A G G T T C
GENFRa1.orf 929 G C A G C A C A G T G G G A A C G A C T A G A A G A G T G C T T G A A T T C T T G A A T T T C
GENFRa2.orf 974 G T C G T G G C A G C G G G A A C A T G G A G G A G G A G T G T G A G A A G T T C T C A G G G A C

DNA48613.orf 1003 T T C T C C C A C A A C C C C T G C C T C A C G G A G G C C A T T G C A G C T A A G A T G C G T T T
GENFRa1.orf 979 T T C A A G G A C A A T A C A T G T C T T A A A A T G C A A T T C A A G C C T T T G G C A A T G G
GENFRa2.orf 1024 T T C A C C G A G A C C C A T G C C T C G G A C G C C A T C A G G C C T T T G G C A A C G G

FIG. 5C

DNA48613.orf 1053 T C A C A G C C A A C T C T T C T C C C A G G A C T G G C C A C A C C C T A C C T T T G C T G T G A
 GDNFRa1.orf 1029 C T C C G A T G T G A C C G T G T G G C A G C C A G C T T C C C A G T A C A G A C C A C C A C T G
 GDNFRa2.orf 1074 C A C G A C G T G A C G T G T C C C A A A G G C C C C T C G T T C A G G C C A C C C A G G

 DNA48613.orf 1103 T G G C A C A C A G A T G A A A A C C C T G C T G T G A G G C C A C A G C C T G G G T G C C C
 GDNFRa1.orf 1079 C C A C T A C C A C C A C T G C C C T C G G G T T A A G A A C A A C C C T G G G C C A G C A
 GDNFRa2.orf 1124 C C C C T C G G G T G G A G A G A C G C C T T C T T T G C C A G A T G A C C T C A G T G A C A G T

 DNA48613.orf 1153 T C T C T T T C T C C T G C A C G C T T C C C T T G A T T C T G C T C C T G A G C C T A T G G T A
 GDNFRa1.orf 1129 G G G T C T G A G A A T G A A A T T C C A C T C A T G T T T G C C A C C G T G T G C A A A T T T
 GDNFRa2.orf 1174 A C C A G C T T G G G G A C C A G T G T C A T C A C C A C C T G C A C G T C T G T C C A G G A G C A

 DNA48613.orf 1203 G
 GDNFRa1.orf 1179 A C A G G C A C A G A A G C T G A A A T C C A A T G T G T C G G G C A A T A C A C A C C T C T G T A
 GDNFRa2.orf 1224 G G G G C T G A A G G C C A A C A A C T C C A A A G A G T T A A G C A T G T G C T T C A C A G A G C

 GDNFRa1.orf 1229 T T T C C A A T G G T A A T T A T G A A A A G A A G G T C T C G T G C T T C C A G C C A C A T A
 GDNFRa2.orf 1274 T C A C G A C A A A T A T C A T C C C A G G G A G T A A C A A G G T G A T C A A A C C T A A C T C A

 GDNFRa1.orf 1279 A C C A C A A A T C A A T G G C T G C T C T C C A A G C T G T G G T C T G A G C C C A C T G C T
 GDNFRa2.orf 1324 G G C C C A G C A G A G C C A G A C C G T C G G C T G C C T T G A C C G T G C T G T C T G T C C T

 GDNFRa1.orf 1329 G G T C C T G T G T A A C C G C T C T G T C C A C C C T A T T A T C T T T A C A G A A A C A T
 GDNFRa2.orf 1374 G A T G C T G A A C A G G C C T T G T A G

 GDNFRa1.orf 1379 C A T A G

FIG. 5D

[illegible]

FIG. 6

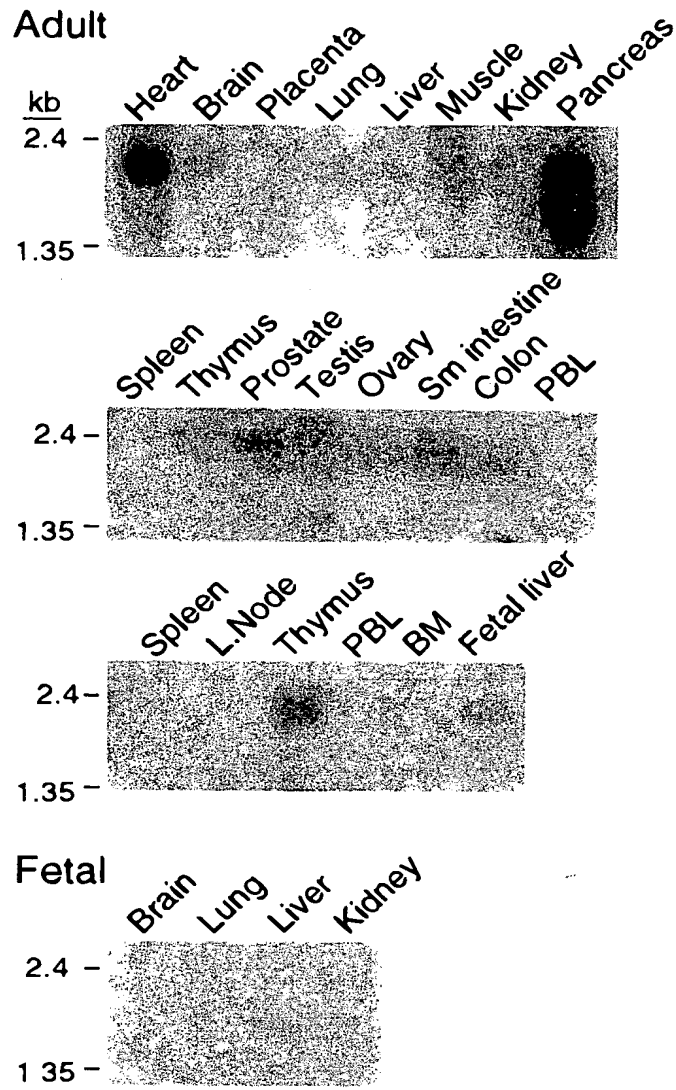


FIG. 7

BEST AVAILABLE COPY

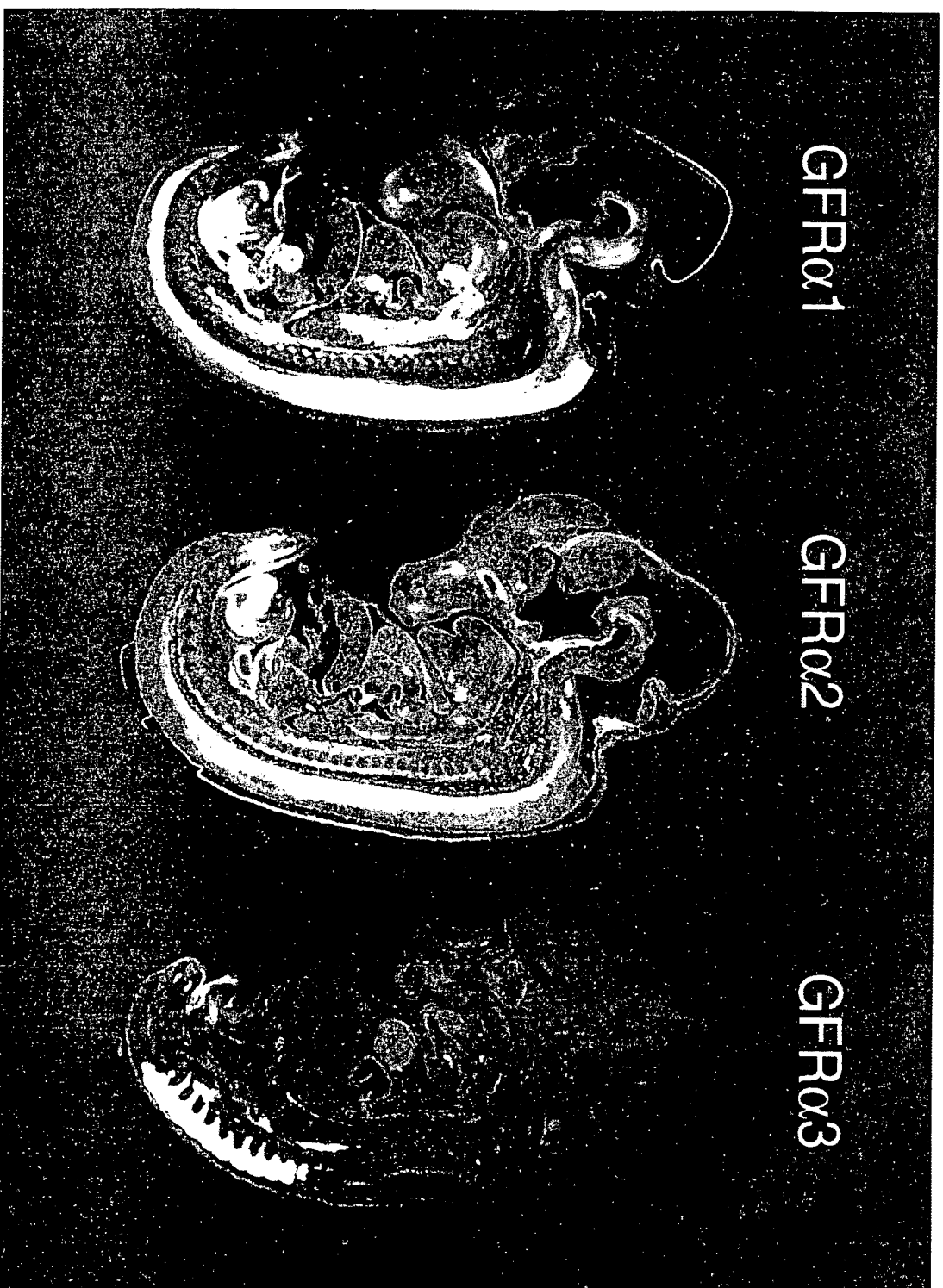
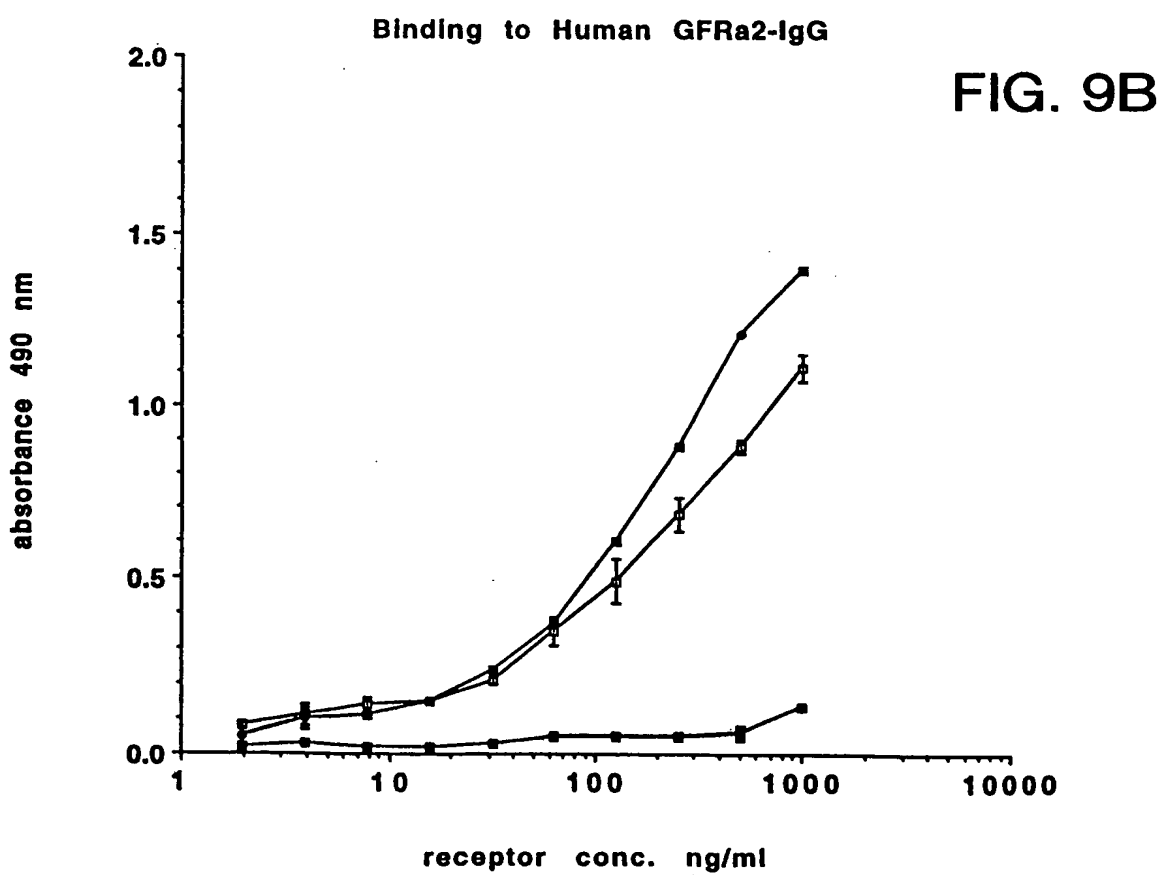
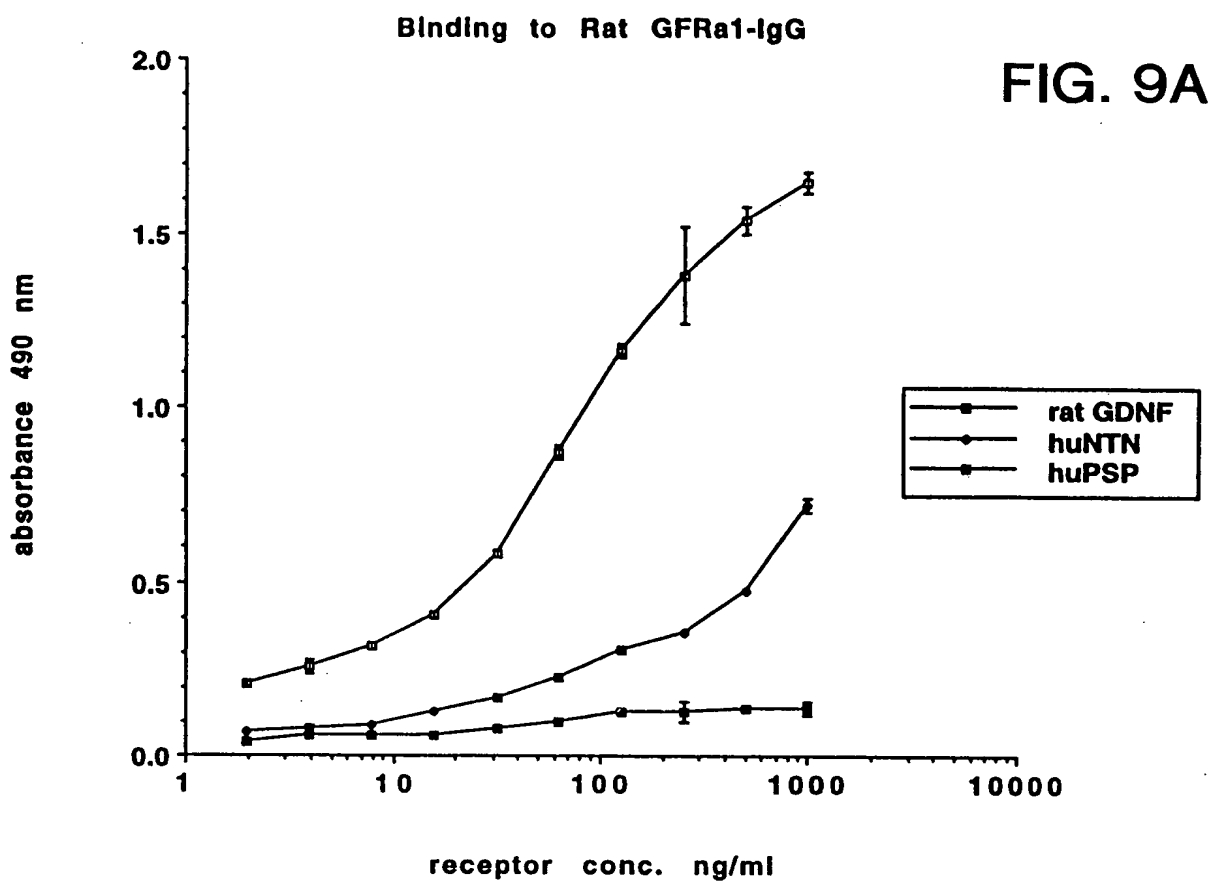


FIG. 8



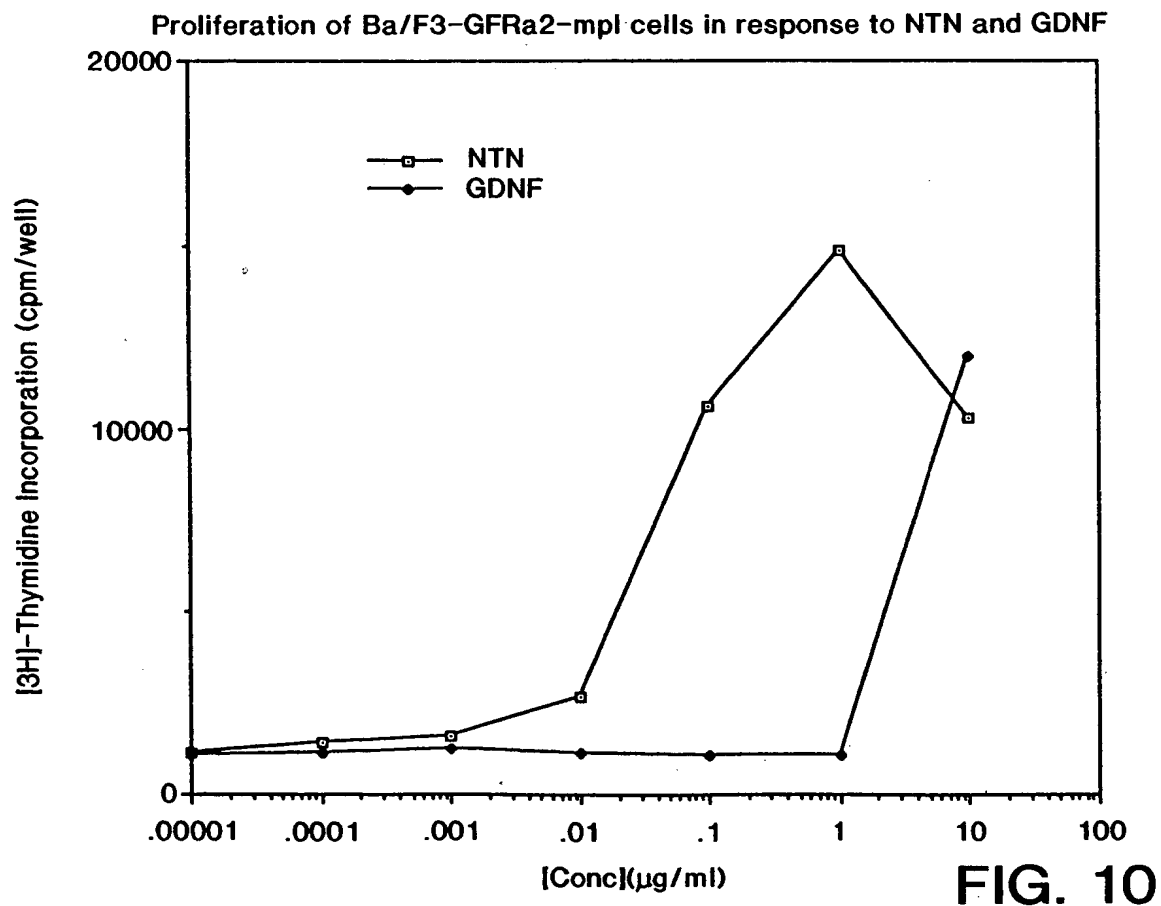
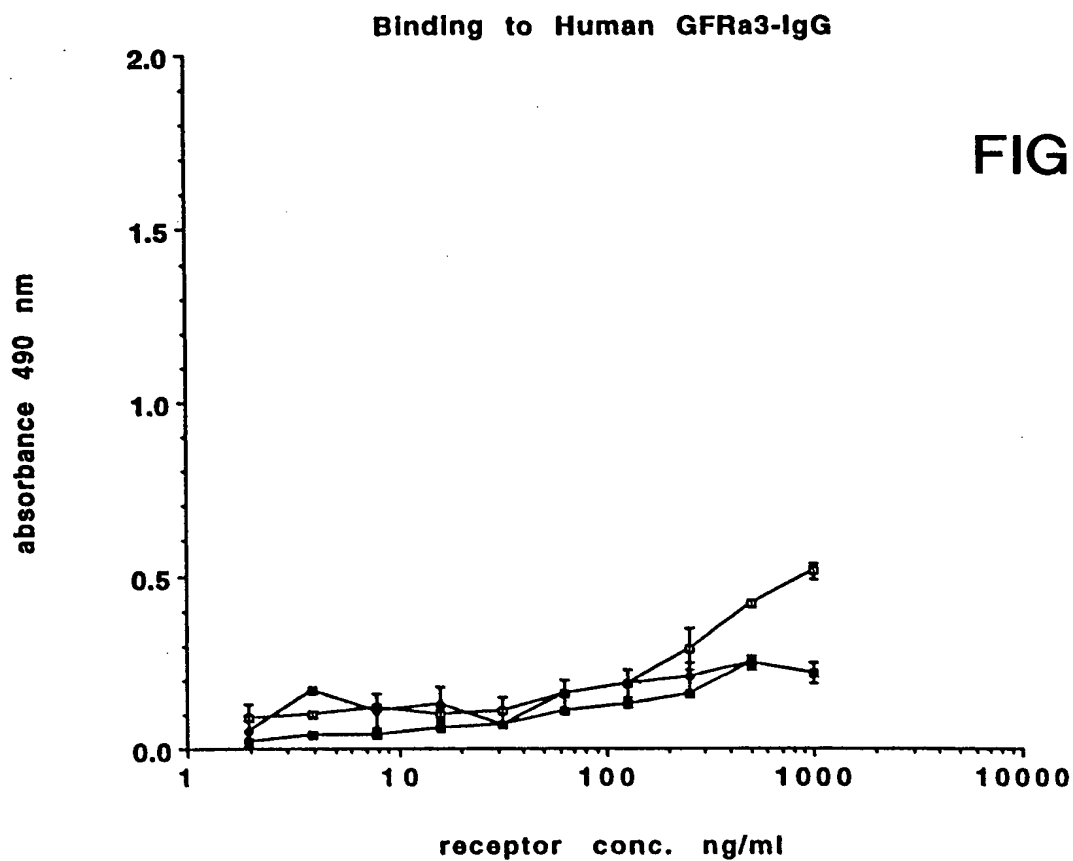


FIG. 10

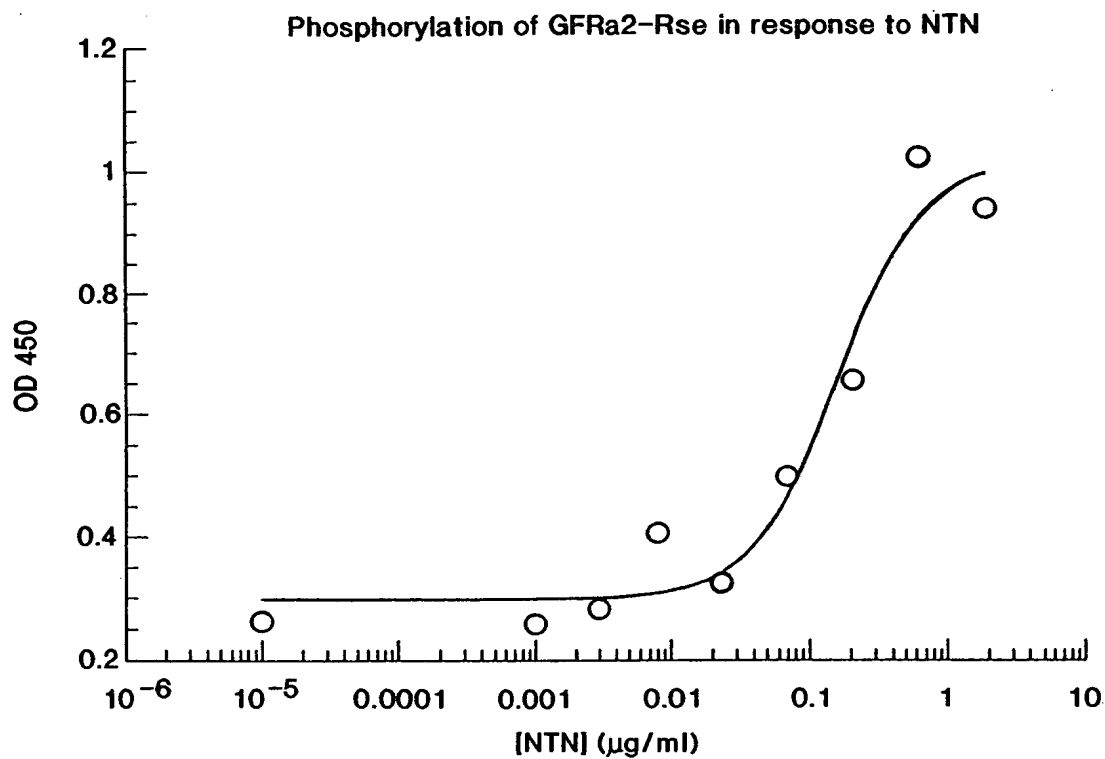


FIG. 11

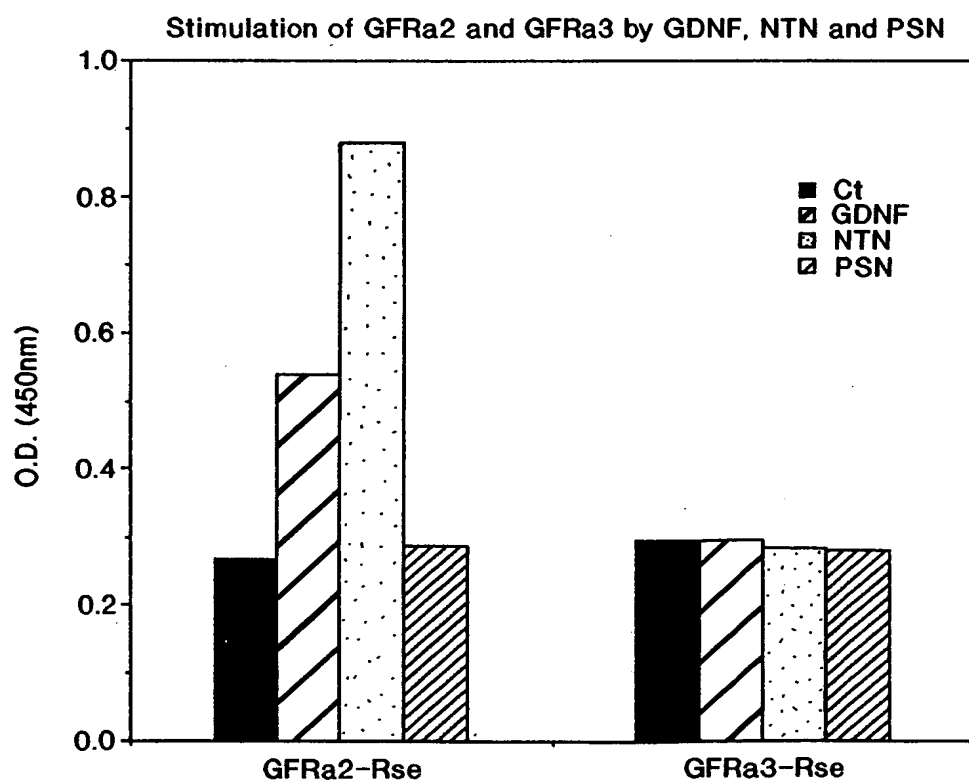


FIG. 12

Agonistic activity of anti gD mAbs in gD-alpha2-rse KIRA

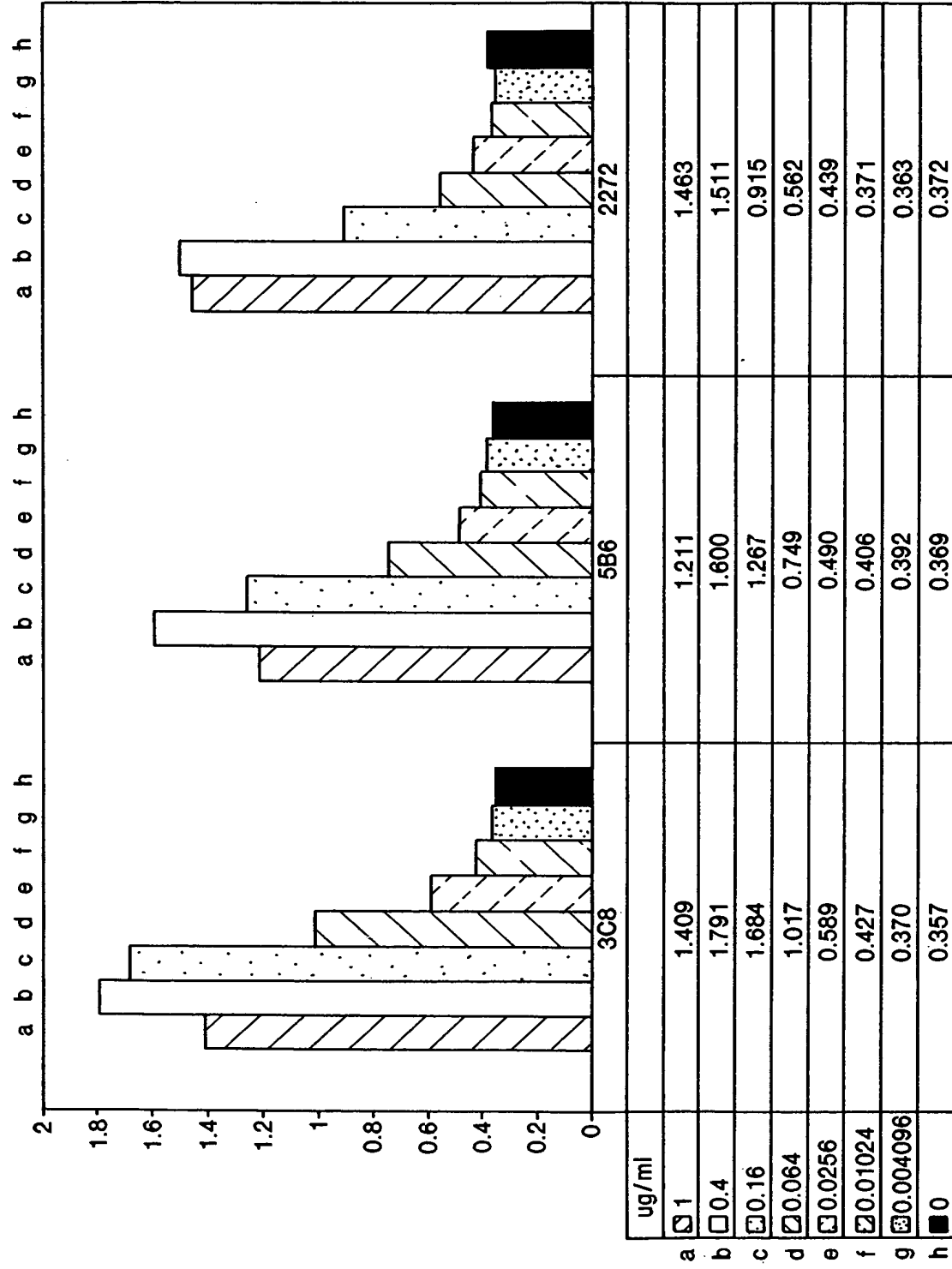


FIG. 13